FIG. 1 Promyostatin

1	MQKLQLCVYI	YLFMLIVAGP	VDLNENSEQK	ENVEKEGLCN	40
41	ACTWRQNTKS	SRIEAIKIQI	LSKLRLETAP	NISKDVIRQL	80
81	LPKAPPLREL	IDQYDVQRDD	SSDGSLEDDD	YHATTETIIT	120
121	MPTESDFLMQ	VDGKPKCCFF	KFSSKIQYNK	VVKAQLWIYL	160
161	RPVETPTTVF	VQILRLIKPM	KDGTRYTGIR	SLKLDMNPGT	200
201	GIWQSIDVKT	VLQNWLKQPE	SNLGIEIKAL	DENGHDLAVT	240
241	FPGPGEDGLN	PFLEVKVTDT	PKRSRR**DFGL**	**DCDEHSTESR**	280
281	**CCRYPLTVDF**	**EAFGWDWIIA**	**PKRYKANYCS**	**GECEFVFLQK**	320
321	**YPHTHLVHQA**	**NPRGSAGPCC**	**TPTKMSPINM**	**LYFNGKEQII**	360
361	**YGKIPAMVVD**	**RCGCS** 376	(SEQ ID NO:1)		

FIG. 2   Mature Myostatin (Human, murine, rat, chicken)

1	DFGLDCDEHS	TESRCCRYPL	TVDFEAFGWD	WIIAPKRYKA	40
41	NYCSGECEFV	FLQKYPHTHL	VHQANPRGSA	GPCCTPTKMS	80
81	PINMLYFNGK	EQIIYGKIPA	MVVDRCGCS 109 (SEQ ID NO:2)		

FIG. 3   Myostatin Homology with GDF-11

```
Myostatin  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYK
Consensus  -+GLDCDEHS+ESRCCRYPLTVDFEAFGWDWIIAPKRYK
GDF-11     NLGLDCDEHSSESRCCRYPLTVDFEAFGWDWIIAPKRYK

Myostatin  ANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTK
Consensus  ANYCSG+CE++F+QKYPHTHLV-QANPRGSAGPCCTPTK
GDF-11     ANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTK

Myostatin  MSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109 (SEQ ID NO:2)
Consensus  MSPINMLYFN-K+QIIYGKIP+MVVDRCGCS      (SEQ ID NO:39)
GDF-11     MSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 108 (SEQ ID NO:40)
```

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Figure 4   Fab Light Chain Variable Region Alignment

FAb   1   CDR1   40
3   QIVLTQSPAI MSASPGEKVT MTC**SASSSIS** **YMH**WYQQKPG
5   QVVLTQSPAI MSASLGEKVT MTC**SASSSVH** **YMH**WYQQKSG
7   QIVLTQSPAI MSASPGEKVT MTC**SASSSIS** **YMH**WYQQKPG
8   QIVLTQSPAI MSASPGEKVT MTC**SASSSVS** **YMH**WYQQKSG
9   QIVLTQSPAI MSASPGEKVT MTC**SASSSVS** **YMH**WYQQKSG
10   QVVLTQSPAI MSASPGEKVT MTC**SASSSIS** **YMH**WYQQKPG
11   QIVLTQSPAI MSASPGEKVT MTC**SASSSIS** **YMH**WYQQKPG
12   QVVLTQSPAI MSASPGEKVT MTC**SASSSVY** **YMH**WYQQRSG
14   QIVLTQSPAI MSASPGEKVT MTC**SASSSVS** **YMH**WYQQKPG
15   QIVLTQSPAI MSASPGEEVT MTC**SASSSIN** **YMH**WYQQKSG
       *   *   *   **   **

FAb   41   CDR2   80
3   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
5   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
7   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
8   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
9   TSPKRWIYDT **SKLAS**GVPVR FSGSGSGTSY SLTISSMEAE
10   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
11   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
12   ASPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
14   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
15   TSPKRWIYDT **SKLAS**GVPAR FSGSGSGTSY SLTISSMEAE
       *

FAb   81   CDR3   108
3   DAATYYC**QQW** **YSNPLT**FGAG TKLELKRAD (SEQ ID NO:3)
5   DAATYYC**QQW** **SSNPLT**FGAG TKLELKRAD (SEQ ID NO:4)
7   DAATYYC**QQW** **YSNPLT**FGAG TKLELKRAD (SEQ ID NO:3)
8   DAATYYC**QQW** **SSNPLT**FGAG TKLELKRAD (SEQ ID NO:5)
9   DAATYYC**QQW** **SRNPLT**FGAG TKLELKRAD (SEQ ID NO:6)
10   DAATYYC**QQW** **YSNPLT**FGAG TKLELKRAD (SEQ ID NO:7)
11   DAATYYC**QQW** **NSNPLT**FGAG TKLELKRAD (SEQ ID NO:8)
12   DAATYYC**QQW** **TYNPLT**FGAG TKLELKRAD (SEQ ID NO:9)
14   DAATYYC**QQW** **YSNPLT**FGAG TKLELKRAD (SEQ ID NO:10)
15   DAATYYC**QQW** **NSNPLT**FGGG TKLELKRAD (SEQ ID NO:11)
                 **   *

Figure 5 Fab Heavy Chain Variable Region Alignment

FAb   1   CDR1   40
```
3      QVTLKESGPG  ILQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
5      QVTLKESGPG  ILQSSQTLSL  TCSFSGFSLS  TSGMSVSWIR
7      QVTLK-SGPG  ILQSSQTLTL  TCSLSGFSLT  TSGMIVSWIR
8      QVTLKESGPG  ILQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
9      QVTLKESGPG  ILQSSQTLSL  TCSVSGFSLS  TSGMSVSWIR
10     QVTLKESGPG  ILQPSQTLSL  TCSLSGFSLR  TSGMSVSWIR
11     QVTLKESGPG  ILQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
12     QVTLKESGPG  MLQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
14     QVTLKESGPG  ILQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
15     QVTLKESGPG  ILQSSQTLSL  TCSLSGFSLR  TSGMSVSWIR
                *           *           *           *       *       *
```

FAb   41   CDR2   80
```
3      QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
5      QSSGKGLEWL  AHIYWDDDKR  YNPSLRSRLT  ISKDTSRNQV
7      QSSGRGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
8      QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
9      QPSGKGLEWL  AHIYWDDDKR  YNPSLKSRLT  ISKDTSRNQV
10     QSSGKGLEWL  AHIYWDDDER  YNPSLRNRLT  ISKDTLRNQV
11     QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
12     QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
14     QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
15     QSSGKGLEWL  AHIYWDDDKR  YNPSLRNRLT  ISKDTLRNQV
                *                       *           * *               *
```

FAb   81   CDR3
```
3      FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
5      FLKITSVDTADTATYYCARRGITTVLGGGTMDYWGQGTSVTVSS
7      FLWISSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
8      FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
9      FLKITSVDTADTATYYCARRAITTVLGGGTMDYWGQGTSVTVSS
10     FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
11     FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
12     FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
14     FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
15     FLKITSVGTADTATYYCARRAITTVIGGGTMDYWGQGTSVTVSS
              *   *   *               *       *
3      (SEQ ID NO:12)
5      (SEQ ID NO:13)
7      (SEQ ID NO:14)
8      (SEQ ID NO:12)
9      (SEQ ID NO:15)
10     (SEQ ID NO:17)
11     (SEQ ID NO:12)
12     (SEQ ID NO:16)
14     (SEQ ID NO:12)
15     (SEQ ID NO:12)
```